Fungal Diversity of Forest Soils as Revealed by Molecular Biological Methods Based on 18S rRNA Gene. (S07-he015608-Oral)

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Abstract:

Soil samples were collected from two contrast forest ecosystems (natural and hoop pine plantation) located at the long-term experimental site in subtropical Queensland, Australia. Microbial DNA in the soil samples were extracted and amplified through polymerase chain reaction (PCR) with fungal-specific primers based on 18S rRNA gene. The PCR products were used for further study by temperature gradient gel electrophoresis (TGGE) and single-strand conformation polymorphism (SSCP). Selected 18S rDNA PCR products (530bp) were also cloned and sequenced. TGGE and SSCP analyses of the PCR products showed clear banding patterns for different samples indicating the different fungal diversity of the soil samples from the two contrasting forest ecosystems. Cloning and sequencing analyses produced 26 different sequences, with 12 from the natural forest and 14 from the hoop pine plantation soil samples. Comparing the clone sequences with the Genebank database showed that all the sequences were from fungi, mostly from wood-decaying fungi or from sludge and other environmental samples.

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